```
RAW SEQUENCE LISTING              DATE: 06/26/2002
PATENT APPLICATION:  US/09/439,311B    TIME: 11:38:13

Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\06262002\I439311B.raw

     8 <110> APPLICANT: Guerry, Patricia
     9        Trust, Trevor J
    10        Burg, Edward
    11        Lee, Lanfong
    13 <120> TITLE OF INVENTION: A Recombinant Polypeptide for use in the Manufacture of
Vaccines
    14        against Campylobacter Induced Diarrhea and to Reduce Colonization
    16 <130> FILE REFERENCE: 78560
    18 <140> CURRENT APPLICATION NUMBER: 09/439,311B
C--> 20 <141> CURRENT FILING DATE: 2001-12-18
    22 <150> PRIOR APPLICATION NUMBER: US 60/108,114
    24 <151> PRIOR FILING DATE: 1998-11-12
    26 <160> NUMBER OF SEQ ID NOS: 6
    28 <170> SOFTWARE: Apple Macintosh Microsoft Word 6.0
    30 <210> SEQ ID NO: 1
    31 <211> LENGTH: 999
    32 <212> TYPE: DNA
    33 <213> ORGANISM: Campylobacter coli
W--> 34 <220> FEATURE:
    35 <223> OTHER INFORMATION:
W--> 36 <400> SEQUENCE: 1
    37 attaacacaa atgttgcagc attaaatgct aaagcaaatt cggatctaaa cagcagagca 60
    38 ttagatcaat cactttcaag actcagttca ggtcttagaa tcaactccgc agcagatgat 120
    39 gcttcaggga tggcgatagc agatagttta agatctcagg caaatacttt gggtcaggct 180
    40 atatctaatg gtaatgatgc tttaggtatc ttgcaaactg cagataaggc tatggatgag 240
    41 caacttaaaa tcttagatac catcaagact aaagcgactc aagctgctca agatggtcaa 300
    42 agcttaaaaa caagaactat gcttcaagca gacatcaacc gtttgatgga agaacttgat 360
    43 aatatcgcaa ataccacttc atttaatggc aaacaacttt aagtggtgg ttttaccaat 420
    44 caagaattcc aaatcggttc aagttcaaat caaactatta aagcaagtat aggagcaact 480
    45 cagtcttcta aaatcggtgt aacaagattt gaaacaggtt cacaaagttt ttcttcaggc 540
    46 actgtaggac ttactattaa aaactacaac ggtatcgaag attttaaatt tgatagtgta 600
    47 gtgatttcta cttcagtagg aacaggtctt ggagctttgg ctgaagagat caacagaaat 660
    48 gcagataaaa caggaattcg tgcaactttt gatgtaaaat ctgtaggagc ctatgcaata 720
    49 aaagcaggaa atacttctca ggattttgct atcaatgggg ttgttatagg taaggttgat 780
    50 tattcagatg gtgatgagaa tggttctttta atttcagcta tcaatgctgt aaaagataca 840
    51 actggtgttc aagcctctaa agatgaaaat ggtaaacttg ttcttacttc ggccgatggt 900
    52 agagggatta aaatcacagg tagcataggt gtaggagctg gtatattgca cactgaaaat 960
    53 tatggaaggt tatctttagt taaaaatgat ggtagagat           999
    56 <210> SEQ ID NO: 2
    57 <211> LENGTH: 333
    58 <212> TYPE: PRT
    59 <213> ORGANISM: Campylobacter coli
W--> 60 <220> FEATURE:
    61 <223> OTHER INFORMATION:
```

RAW SEQUENCE LISTING                    DATE: 06/26/2002
PATENT APPLICATION:   US/09/439,311B       TIME: 11:38:13

Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\06262002\I439311B.raw

W--> 62 <400> SEQUENCE: 2
    63 Ile Asn Thr Asn Val Ala Ala Leu Asn Ala Lys Ala Asn Ser Asp
    64 1               5               10              15
    65 Leu Asn Ser Arg Ala Leu Asp Gln Ser Leu Ser Arg Leu Ser Ser
    66             20              25              30
    67 Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala Ser Gly Met Ala
    68             35              40              45
    69 Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr Leu Gly Gln Ala
    70             50              55              60
    71 Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu Gln Thr Ala Asp
    72             65              70              75
    73 Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Ile Lys Thr
    74             80              85              90
    75 Lys Ala Thr-Gln Ala Ala Gln Asp Gly Gln Ser Leu Lys Thr Arg
    76             95              100             105
    77 Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met Glu Glu Leu Asp
    78             110             115             120
    79 Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys Gln Leu Leu Ser
    80             125             130             135
    81 Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly Ser Ser Ser Asn
    82             140             145             150
    83 Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln Ser Ser Lys Ile
    84             155             160             165
    85 Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser Phe Ser Ser Gly
    86             170             175             180
    87 Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly Ile Glu Asp Phe
    88             185             190             195
    89 Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val Gly Thr Gly Leu
    90             200             205             210
    91 Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala Asp Lys Thr Gly
    92             215             220             225
    93 Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly Ala Tyr Ala Ile
    94             230             235             240
    95 Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile Asn Gly Val Val
    96             245             250             255
    97 Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu Asn Gly Ser Leu
    98             260             265             270
    99 Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr Gly Val Gln Ala
   100             275             280             285
   101 Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr Ser Ala Asp Gly
   102             290             295             300
   103 Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val Gly Ala Gly Ile
   104             305             310             315
   105 Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu Val Lys Asn Asp
   106             320             325             330
   107 Gly Arg Asp
   109 <210> SEQ ID NO: 3
   111 <211> LENGTH: 27
   112 <212> TYPE: DNA

```
        113 <213> ORGANISM: Campylobacter coli
W--> 114 <220> FEATURE:
        115 <223> OTHER INFORMATION:
W--> 116 <400> SEQUENCE: 3
        117 accaatatta acacaaatgt tgcagca                              27
        119 <210> SEQ ID NO: 4
        121 <211> LENGTH: 33
        122 <212> TYPE: DNA
        123 <213> ORGANISM: Campylobacter coli
W--> 124 <220> FEATURE:
        125 <223> OTHER INFORMATION:
W--> 126 <400> SEQUENCE: 4
        127 ttatctagac taatctctac catcattttt aac                       33
        129 <210> SEQ ID NO: 5
        131 <211> LENGTH: 574
        132 <212> TYPE: PRT
        133 <213> ORGANISM: Campylobacter jejuni 81-176
W--> 134 <220> FEATURE:
        135 <223> OTHER INFORMATION:
W--> 136 <400> SEQUENCE: 5
        137 Met Gly Phe Arg Ile Asn Thr Asn Val Ala Ala Leu Asn Ala Lys
        138 1               5                   10                  15
        139 Ala Asn Ser Asp Leu Asn Ser Arg Ala Leu Asp Gln Ser Leu Ser
        140                 20                  25                  30
        141 Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala
        142                 35                  40                  45
        143 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr
        144                 50                  55                  60
        145 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu
        146                 65                  70                  75
        147 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp
        148                 80                  85                  90
        149 Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser
        150                 95                  100                 105
        151 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met
        152                 110                 115                 120
        153 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys
        154                 125                 130                 135
        155 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly
        156                 140                 145                 150
        157 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln
        158                 155                 160                 165
        159 Ser Ser Lys Ile Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser
        160                 170                 175                 180
        161 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly
        162                 185                 190                 195
        163 Ile Glu Asp Phe Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val
        164                 200                 205                 210
        165 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala
```

```
166                  215                  220                  225
167 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly
168                  230                  235                  240
169 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile
170                  245                  250                  255
171 Asn Gly Val Val Ile Gly Gln Ile Asn Tyr Asn Asp Gly Asp Asn
172                  260                  265                  270
173 Asn Gly Gln Leu Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr
174                  275                  280                  285
175 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr
176                  290                  295                  300
177 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val
178                  305                  310                  315
179 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu
180                  320                  325                  330
181 Val Lys Asn Asp Gly Arg Asp Ile Asn Ile Ser Gly Thr Gly Leu
182                  335                  340                  345
183 Ser Ala Ile Gly Met Gly Ala Thr Asp Met Ile Ser Gln Ser Ser
184                  350                  355                  360
185 Val Ser Leu Arg Glu Ser Lys Gly Gln Ile Ser Ala Ala Asn Ala
186                  365                  370                  375
187 Asp Ala Met Gly Phe Asn Ser Tyr Lys Gly gly Gly Lys Phe Val
188                  380                  385                  390
189 Phe Thr Gln Asn Val Ser Ser Ile Ser Ala Phe Met Ser Ala Gln
190                  395                  400                  405
191 Gly Ser Gly Phe Ser Arg Gly Ser Gly Phe Ser Val Gly Ser Gly
192                  410                  415                  420
193 Lys Asn Leu Ser Val Gly Leu Ser Gln Gly Ile Gln Ile Ile Ser
194                  425                  430                  435
195 Ser Ala Ala Ser Met Ser Asn Thr Tyr Val Val Ser Ala Gly Ser
196                  440                  445                  450
197 Gly Phe Ser Ser Gly Ser Gly Asn Ser Gln Phe Ala Ala Leu Lys
198                  455                  460                  465
199 Thr Thr Ala Ala Asn Thr Thr Asp Glu Thr Ala gly Val Thr Thr
200                  470                  475                  480
201 Leu Lys Gly Ala Met Ala Val Met Asp Ile Ala Glu Thr Ala Ile
202                  485                  490                  495
203 Thr Asn Leu Asp Gln Ile Arg Ala Asp Ile Gly Ser Ile Gln Asn
204                  500                  505                  510
205 Gln Val Thr Ser Thr Ile Asn Asn Ile Thr Val Thr Gln Val Asn
206                  515                  520                  525
207 Val Lys Ala Ala Glu Ser Gln Ile Arg Asp Val Asp Phe Ala Ser
208                  530                  535                  540
209 Glu Ser Ala Asn Tyr Ser Lys Ala Asn Ile Leu Ala Gln Ser Gly
210                  545                  550                  555
211 Ser Tyr Ala Met Ala Gln Ala Asn Ser Ser Gln Gln Asn Val Leu
212                  560                  565                  570
213 Arg Leu Leu Gln
215 <210> SEQ ID NO: 6
```

RAW SEQUENCE LISTING                    DATE: 06/26/2002
PATENT APPLICATION:  US/09/439,311B      TIME: 11:38:13

Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\06262002\I439311B.raw

```
217 <211> LENGTH: 573
218 <212> TYPE: PRT
219 <213> ORGANISM: Campylobacter coli VC167 T2
W--> 220 <220> FEATURE:
221 <223> OTHER INFORMATION:
W--> 222 <400> SEQUENCE: 6
223 Met Gly Phe Arg Ile Asn Thr Asn Val Ala Ala Leu Asn Ala Lys
224 1               5                   10                  15
225 Ala Asn Ser Asp Leu Asn Ser Arg Ala Leu Asp Gln Ser Leu Ser
226                 20                  25                  30
227 Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala
228                 35                  40                  45
229 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr
230                 50                  55                  60
231 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu
232                 65                  70                  75
233 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp
234                 80                  85                  90
235 Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser
236                 95                  100                 105
237 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met
238                 110                 115                 120
239 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys
240                 125                 130                 135
241 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly
242                 140                 145                 150
243 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln
244                 155                 160                 165
245 Ser Ser Lys Ile Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser
246                 170                 175                 180
247 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly
248                 185                 190                 195
249 Ile Glu Asp Phe Lys Phe Gln Ser Val Val Ile Ser Thr Ser Val
250                 200                 205                 210
251 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala
252                 215                 220                 225
253 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly
254                 230                 235                 240
255 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile
256                 245                 250                 255
257 Asn Gly Val Val Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu
258                 260                 265                 270
259 Asn Gly Ser Leu Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr
260                 275                 280                 285
261 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr
262                 290                 295                 300
263 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val
264                 305                 310                 315
265 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu
```

**VERIFICATION SUMMARY**          DATE: 06/26/2002
PATENT APPLICATION:  US/09/439,311B          TIME: 11:38:14

Input Set : **A:\PTO.AMC.TXT**
Output Set: **N:\CRF3\06262002\I439311B.raw**

```
L:20  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34  M:283 W: Missing Blank Line separator, <220> field identifier
L:36  M:283 W: Missing Blank Line separator, <400> field identifier
L:60  M:283 W: Missing Blank Line separator, <220> field identifier
L:62  M:283 W: Missing Blank Line separator, <400> field identifier
L:114 M:283 W: Missing Blank Line separator, <220> field identifier
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:124 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:220 M:283 W: Missing Blank Line separator, <220> field identifier
L:222 M:283 W: Missing Blank Line separator, <400> field identifier
```